



## SEQUENCE LISTING

<110> IRM, LLC and Novartis Pharmaceuticals Corporation  
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Vincent, Fabien  
Cueto, Maria A

<120> HIGHLY SPECIFIC MODULATORS OF GTPASES FOR TARGET VALIDATION

<130> 36-001720US

<140> US 10/660,113

<141> 2003-09-10

<160> 52

<170> PatentIn version 3.2

<210> 1

<211> 189

<212> PRT

<213> Homo sapiens

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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
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Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser

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Ser Ala Ala Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
 20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
 35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
 50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
 65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
 85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
 100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
 115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
 130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
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Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
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Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
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Ser Ala Gly Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

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Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
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<223> mutant of H-Ras

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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Ala Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
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Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
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<223> mutant of H-Ras

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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Gly Val Asp Glu Tyr  
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Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
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Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
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Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Ala Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

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165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Gly Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Ala Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys

1	5	10	15
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Asp Pro Thr	Ile Glu Asp Ser	Tyr Arg Lys Gln Val	Val Ile Asp Gly
35	40	45	
Glu Thr Cys Leu Leu	Asp Ile Leu Asp Thr	Ala Gly Gln Glu Glu Tyr	
50	55	60	
Ser Ala Met Arg Asp	Gln Tyr Met Arg Thr	Gly Glu Gly Phe Leu Cys	
65	70	75	80
Val Phe Ala Ile	Asn Asn Thr Lys Ser	Phe Glu Asp Ile His	Gln Tyr
85	90	95	
Arg Glu Gln Ile	Lys Arg Val Lys	Asp Ser Asp Asp Val	Pro Met Val
100	105	110	
Leu Val Gly	Asn Gly Cys Asp	Leu Ala Ala Arg Thr	Val Glu Ser Arg
115	120	125	
Gln Ala Gln Asp	Leu Ala Arg	Ser Tyr Gly Ile	Pro Tyr Ile Glu Thr
130	135	140	
Ser Ala Lys Thr Arg	Gln Gly Val Glu Asp	Ala Phe Tyr Thr Leu	Val
145	150	155	160
Arg Glu Ile Arg	Gln His Lys Leu Arg	Lys Leu Asn Pro Pro	Asp Glu
165	170	175	
Ser Gly Pro Gly	Cys Met Ser Cys	Lys Cys Val Leu Ser	
180	185		

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<220>  
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Met Thr Glu Tyr	Lys Leu Val Val Val	Gly Ala Gly Gly Val	Gly Lys
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Ser Ala Ala Thr	Ile Gln Leu Ile	Gln Asn His Phe Val	Asp Glu Tyr
20	25	30	
Asp Pro Thr	Ile Glu Asp Ser	Tyr Arg Lys Gln Val	Val Ile Asp Gly
35	40	45	
Glu Thr Cys Leu Leu	Asp Ile Leu Asp Thr	Ala Gly Gln Glu Glu Tyr	



50

55

60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Ala Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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<220>  
<223> mutant of H-Ras

<400> 11

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Ala Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val

100	105	110
Leu Val Gly Gly Lys Cys Asp	Leu Ala Ala Arg Thr	Val Glu Ser Arg
115	120	125
Gln Ala Gln Asp Leu Ala Arg	Ser Tyr Gly Ile Pro Tyr Ile Glu Thr	
130	135	140
Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val		
145	150	155
Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu		
165	170	175
Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser		
180	185	

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<220>  
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<400> 12

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys	
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Ser Ala Gly Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr	
20	25
Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly	
35	40
Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr	
50	55
Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys	
65	70
Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr	
85	90
Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val	
100	105
Leu Val Gly Ala Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg	
115	120
Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr	
130	135
Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val	

145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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<400> 13

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Gly Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Gly Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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<220>  
<223> mutant of H-Ras

<400> 14

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Cys Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Ala Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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<400> 15

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Cys Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Gly Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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<400> 16

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Cys Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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<400> 17

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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Gly Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Cys  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

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cggaagcagg tgggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
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cggaaacagg tgggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc	180
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gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc	420
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cggaaacagg tgggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc	180
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt	240
gtgtttgcca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc	300
aaacgggtga aggactcggg tgacgtgccc atggtgctgg tggggaacaa gtgtgacctg	360
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc	420
tacatcgaga cctcggccaa gacccggcag ggagtggagg atgccttcta cacgttggtg	480
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc	540
tgcattgagct gcaagtgtgt gctctcctga	570

<210> 22  
 <211> 570



<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 22  
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cggaagcagg tgggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgccca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300  
aaacgggtga aggactcgga tgacgtgccc atggtgctgg tggggaacaa gtgtgacctg 360  
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgaga cctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcattgagct gcaagtgtgt gctctcctga 570

<210> 23  
<211> 570  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 23  
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cggaagcagg tgggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgccca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300  
aaacgggtga aggactcgga tgacgtgccc atggtgctgg tgggggcaa gtgtgacctg 360  
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgaga cctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcattgagct gcaagtgtgt gctctcctga 570

<210> 24  
<211> 504  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 24  
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atccagctga tccagaacca ttttgtggac gaatacgacc ccactataga ggattcctac 120

cggaagcagg	tgggtcattga	tggggagacg	tgctgtttg	acatcctgga	taccgccggc	180
caggaggagt	acagcgccat	gcgggaccag	tacatgcgca	ccggggaggg	cttcctgtgt	240
gtgtttgcca	tcaacaacac	caagtctttt	gaggacatcc	accagtacag	ggagcagatc	300
aaacgggtga	aggactcgga	tgacgtgccc	atggtgctgg	tggggggcaa	gtgtgacctg	360
gctgcacgca	ctgtggaatc	tcggcaggct	caggacctcg	cccgaagcta	cggcatcccc	420
tacatcgaga	cctcggccaa	gacccggcag	ggagtggagg	atgccttcta	cacgttggtg	480
cgtgagatcc	ggcagcacia	gctg				504

<210> 25  
 <211> 504  
 <212> DNA  
 <213> artificial

<220>  
 <223> mutant of H-Ras

<400> 25						
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cggaagcagg	tgggtcattga	tggggagacg	tgctgtttg	acatcctgga	taccgccggc	180
caggaggagt	acagcgccat	gcgggaccag	tacatgcgca	ccggggaggg	cttcctgtgt	240
gtgtttgcca	tcaacaacac	caagtctttt	gaggacatcc	accagtacag	ggagcagatc	300
aaacgggtga	aggactcgga	tgacgtgccc	atggtgctgg	tggggaacgc	gtgtgacctg	360
gctgcacgca	ctgtggaatc	tcggcaggct	caggacctcg	cccgaagcta	cggcatcccc	420
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cgtgagatcc	ggcagcacia	gctg				504

<210> 26  
 <211> 504  
 <212> DNA  
 <213> artificial

<220>  
 <223> mutant of H-Ras

<400> 26						
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cggaagcagg	tgggtcattga	tggggagacg	tgctgtttg	acatcctgga	taccgccggc	180
caggaggagt	acagcgccat	gcgggaccag	tacatgcgca	ccggggaggg	cttcctgtgt	240
gtgtttgcca	tcaacaacac	caagtctttt	gaggacatcc	accagtacag	ggagcagatc	300
aaacgggtga	aggactcgga	tgacgtgccc	atggtgctgg	tggggaacgg	gtgtgacctg	360
gctgcacgca	ctgtggaatc	tcggcaggct	caggacctcg	cccgaagcta	cggcatcccc	420
tacatcgaga	cctcggccaa	gacccggcag	ggagtggagg	atgccttcta	cacgttggtg	480
cgtgagatcc	ggcagcacia	gctg				504

<210> 27  
<211> 570  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

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cggaagcagg tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgccca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300  
aaacgggtga aggactcgga tgacgtgccc atggtgctgg tggggggcaa gtgtgacctg 360  
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgaga cctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcattgagct gcaagtgtgt gctctcctga 570

<210> 28  
<211> 570  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 28  
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cggaagcagg tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
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gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgaga cctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcattgagct gcaagtgtgt gctctcctga 570

<210> 29  
<211> 570  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 29  
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cggaagcagg tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgcca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300  
aaacgggtga aggactcgga tgacgtgccc atggtgctgg tggggggcaa gtgtgacctg 360  
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgaga cctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcatgagct gcaagtgtgt gctctcctga 570

<210> 30  
<211> 570  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 30  
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cggaagcagg tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgcca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300  
aaacgggtga aggactcgga tgacgtgccc atggtgctgg tggggggcaa gtgtgacctg 360  
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgaga cctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcatgagct gcaagtgtgt gctctcctga 570

<210> 31  
<211> 570  
<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 31  
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cggaagcagg tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgcca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300

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tacatcgaga	cctcggccaa	gacccggcag	ggagtggagg	atgccttcta	cacgttggtg	480
cgtgagatcc	ggcagcacia	gctgcggaag	ctgaaccctc	ctgatgagag	tggccccggc	540
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<210> 32  
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 <212> DNA  
 <213> artificial

<220>  
 <223> mutant of H-Ras

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cggaaagcagg	tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180
caggaggagt	acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240
gtgtttgcca	tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300
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tacatcgaga	cctcggccaa gacccggcag ggagtggagg atgccttcta cacgttggtg 480
cgtgagatcc	ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540
tgcatagact	gcaagtgtgt gctctcctga 570

<210> 33  
 <211> 570  
 <212> DNA  
 <213> artificial

<220>  
 <223> mutant of H-Ras

<400> 33	
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cggaaagcagg	tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180
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tacatcgaga	cctcggccaa gacccggcag ggagtggagg atgccttcta cacgttggtg 480
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tgcatagact	gcaagtgtgt gctctcctga 570

<210> 34  
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<212> DNA  
<213> artificial

<220>  
<223> mutant of H-Ras

<400> 34  
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cggaagcagg tggtcattga tggggagacg tgcctgttgg acatcctgga taccgccggc 180  
caggaggagt acagcgccat gcgggaccag tacatgcgca ccggggaggg cttcctgtgt 240  
gtgtttgcca tcaacaacac caagtctttt gaggacatcc accagtacag ggagcagatc 300  
aaacgggtga aggactcgga tgacgtgccc atggtgctgg tggggggcaa gtgtgacctg 360  
gctgcacgca ctgtggaatc tcggcaggct caggacctcg cccgaagcta cggcatcccc 420  
tacatcgagt gctcggccaa gaccggcag ggagtggagg atgccttcta cacgttggtg 480  
cgtgagatcc ggcagcacia gctgcggaag ctgaaccctc ctgatgagag tggccccggc 540  
tgcattgagct gcaagtgtgt gctctcctga 570

<210> 35  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 35  
Gly Ala Gly Gly Val Gly Lys Ser Ala Leu Thr Ile  
1 5 10

<210> 36  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 36  
Leu Val Gly Asn Lys Cys Asp  
1 5

<210> 37  
<211> 12  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 37  
Gly Asp Ser Gly Val Gly Lys Thr Ser Leu Met Asn  
1 5 10

<210> 38  
<211> 7

<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 38

Val Leu Gly Asn Lys Ile Asp  
1 5

<210> 39  
<211> 12  
<212> PRT  
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<220>  
<223> unknown species

<400> 39

Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys  
1 5 10

<210> 40  
<211> 7  
<212> PRT  
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<220>  
<223> unknown species

<400> 40

Leu Cys Gly Asn Lys Val Asp  
1 5

<210> 41  
<211> 12  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 41

Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Leu  
1 5 10

<210> 42  
<211> 7  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 42

Val Val Gly Asn Lys Ser Asp  
1 5

<210> 43  
<211> 12

<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 43

Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Val  
1 5 10

<210> 44  
<211> 7  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 44

Leu Val Gly Asn Lys Cys Asp  
1 5

<210> 45  
<211> 12  
<212> PRT  
<213> Unknown

<220>  
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<400> 45

Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile  
1 5 10

<210> 46  
<211> 7  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 46

Leu Val Gly Asn Lys Lys Asp  
1 5

<210> 47  
<211> 12  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 47

Gly Leu Asp Cys Ala Gly Lys Thr Thr Val Leu Tyr  
1 5 10

<210> 48  
<211> 7



<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 48

Ile Val Ala Asn Lys Gln Asp  
1 5

<210> 49  
<211> 12  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 49

Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys  
1 5 10

<210> 50  
<211> 7  
<212> PRT  
<213> Unknown

<220>  
<223> Unknown species

<400> 50

Leu Phe Leu Asn Lys Lys Asp  
1 5

<210> 51  
<211> 12  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 51

Gly His Val Asp Ser Gly Lys Ser Thr Thr Thr Gly  
1 5 10

<210> 52  
<211> 7  
<212> PRT  
<213> Unknown

<220>  
<223> unknown species

<400> 52

Val Gly Val Asn Lys Met Asp  
1 5